

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 8, 2003, 14:31:47 ; Search time 93 Seconds
(without alignments)
1207.480 Million cell updates/sec

Title: US-09-001-737-8
Perfect score: 545
Sequence: 1 MAKEIKFSADARAAVRCVD.....TPAFAMFGMDPGMGMG 545

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 8

Total number of hits satisfying chosen parameters: 564

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	304	55.8	481	2	03733 streptococc
2	184	33.8	184	2	0916F1 streptococc
3	156	28.6	159	2	08RJH4 streptococc
4	141	25.9	184	2	093TK8 streptococc
5	100	18.3	159	2	08RJH4 streptococc
6	91	16.7	159	2	08RJH4 streptococc
7	86	15.6	184	2	093TK4 streptococc
8	80	14.7	184	2	093TK4 streptococc
9	80	14.7	184	2	093TK4 streptococc
10	80	14.7	184	2	093TK4 streptococc
11	78	14.3	159	2	08RJH4 streptococc
12	78	14.3	184	2	093TK4 streptococc
13	78	14.3	184	2	093TK4 streptococc
14	75	13.8	184	2	093TK4 streptococc
15	70	12.8	540	2	093TK4 streptococc
16	70	12.8	540	2	093TK4 streptococc

17	67	12.3	540	2	08V758 streptococc
18	58	10.6	541	2	093E06 streptococc
19	56	10.3	542	2	09AEP7 streptococc
20	55	10.1	543	2	09KJ23 streptococc
21	47	8.6	184	2	093TK4 streptococc
22	43	7.9	184	2	093TK4 streptococc
23	36	6.6	184	2	093TK4 streptococc
24	36	6.6	184	2	093TK4 streptococc
25	36	6.6	184	2	093TK4 streptococc
26	36	6.6	184	2	093TK4 streptococc
27	36	6.6	184	2	093TK4 streptococc
28	36	6.6	184	2	093TK4 streptococc
29	36	6.6	184	2	093TK4 streptococc
30	36	6.6	184	2	093TK4 streptococc
31	36	6.6	184	2	093TK4 streptococc
32	36	6.6	184	2	093TK4 streptococc
33	36	6.6	184	2	093TK4 streptococc
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35	36	6.6	184	2	093TK4 streptococc
36	36	6.6	184	2	093TK4 streptococc
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49	36	6.6	184	2	093TK4 streptococc
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55	36	6.6	184	2	093TK4 streptococc
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72	36	6.6	184	2	093TK4 streptococc
73	36	6.6	184	2	093TK4 streptococc
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82	36	6.6	184	2	093TK4 streptococc
83	36	6.6	184	2	093TK4 streptococc
84	36	6.6	184	2	093TK4 streptococc
85	36	6.6	184	2	093TK4 streptococc
86	36	6.6	184	2	093TK4 streptococc
87	36	6.6	184	2	093TK4 streptococc
88	36	6.6	184	2	093TK4 streptococc
89	36	6.6	184	2	093TK4 streptococc

236	15	2.8	563	4	096F26	096f26 homo sapien	309	13	2.4	546	2	08RN02	08rn02 helicobacte
237	15	2.8	573	5	0905N2	0905n2 myzus persi	310	13	2.4	565	2	09BLG8	09blg8 paramecium
238	15	2.8	581	5	046219	046219 culicoides	311	13	2.4	575	5	09YI08	09yi08 toxoplasma
239	15	2.8	582	5	0905L7	0905l7 paracetrot	312	13	2.4	596	10	09FHA9	09fha9 arabidopsis
240	15	2.8	598	5	090X77	090x77 onchocerca	313	13	2.4	599	10	09LJE4	09lje4 arabidopsis
241	14	2.6	82	2	09FAF3	09faf3 buchnera ap	314	13	2.4	599	10	09SAV2	09sav2 solanum tub
242	14	2.6	82	2	09FAF1	09faf1 buchnera ap	315	13	2.4	600	10	09SAV2	09sav2 arabidopsis
243	14	2.6	82	2	09FAE9	09fae9 buchnera ap	316	13	2.4	601	10	09LWT6	09lwt6 oryza sativ
244	14	2.6	82	2	09FAE7	09fae7 buchnera ap	317	13	2.4	172	5	09S1G6	09s1g6 tetrahymena
245	14	2.6	82	2	09FAE5	09fae5 buchnera ap	318	13	2.2	184	2	09X2U0	09x2u0 staphylococ
246	14	2.6	82	2	09FAE3	09fae3 buchnera ap	319	13	2.2	185	2	093A38	093a38 leprospira
247	14	2.6	191	2	08V0S2	08vos2 secondary s	320	12	2.2	185	2	08VVC5	08vvc5 anaerobiosp
248	14	2.6	536	2	09VLAS0	09vlas0 desulfiloba	321	12	2.2	356	2	093W74	093w74 anaplasma p
249	14	2.6	538	2	09EZV1	09ezv1 thermotoga	322	12	2.2	374	2	08V548	08v548 wolbachia e
250	14	2.6	550	2	09S303	09s303 rickettsia	323	12	2.2	402	2	09RNM2	09rnm2 anaplasma p
251	14	2.6	550	2	08V017	08v017 rickettsia	324	12	2.2	402	2	0933C9	0933c9 anaplasma p
252	14	2.6	555	2	09X603	09x603 primary end	325	12	2.2	402	2	09R3K9	09r3k9 anaplasma p
253	14	2.6	572	10	09LRW0	09lrw0 arabidopsis	326	12	2.2	405	2	09XBM9	09xbm9 anaplasma p
254	14	2.6	574	3	09P521	09p521 neurospora	327	12	2.2	409	2	09LBM9	09lbm9 anaplasma m
255	14	2.6	594	3	094110	094110 coccidiolide	328	12	2.2	409	2	09LC61	09lc61 ehrlichia s
256	13	2.4	174	10	P93571	P93571 solanum tub	329	12	2.2	410	2	09RM17	09rm17 ehrlichia s
257	13	2.4	181	2	0930J0	093qj0 vibrio sp.	330	12	2.2	410	2	09KJ73	09kj73 desulfiloba
258	13	2.4	183	2	08V014	08v014 bacillus th	331	12	2.2	523	2	08RTT3	08rtt3 anaplasma p
259	13	2.4	184	2	093R47	093r47 bacillus th	332	12	2.2	526	2	0931D1	0931d1 anaplasma p
260	13	2.4	184	2	093R46	093r46 bacillus an	333	12	2.2	526	2	08RTT0	08rtt0 anaplasma p
261	13	2.4	184	2	093R45	093r45 bacillus ce	334	12	2.2	533	2	09S3V5	09s3v5 anaplasma p
262	13	2.4	184	2	0930K6	093qk6 vibrio chol	335	12	2.2	533	2	09S3V5	09s3v5 anaplasma p
263	13	2.4	184	2	0930K5	093qk5 vibrio chol	336	12	2.2	541	2	09S3V5	09s3v5 anaplasma p
264	13	2.4	184	2	0930K2	093qk2 vibrio holi	337	12	2.2	548	16	09RMQ9	09rmq9 anaplasma p
265	13	2.4	184	2	0930K1	093qk1 vibrio holi	338	12	2.2	550	5	P91886	P91886 onchocerca
266	13	2.4	184	2	08V016	08v016 bacillus an	339	12	2.2	552	2	008334	008334 wolbachia s
267	13	2.4	184	2	08V015	08v015 bacillus ce	340	12	2.2	552	2	008334	008334 guillardi
268	13	2.4	185	2	0930K8	093qk8 vibrio harv	341	12	2.2	559	10	09AM01	09am01 guillardi
269	13	2.4	185	2	0930K7	093qk7 vibrio chol	342	12	2.2	589	10	09AM01	09am01 guillardi
270	13	2.4	185	2	0930K4	093qk4 vibrio cnc	343	12	2.2	611	10	09C667	09c667 arabidopsis
271	13	2.4	185	2	0930K3	093qk3 vibrio cnc	344	12	2.0	84	2	093EN7	093en7 mycobacteri
272	13	2.4	185	2	0930K1	093qk1 vibrio fluv	345	11	2.0	84	2	093EN6	093en6 mycobacteri
273	13	2.4	185	2	0930K0	093qk0 vibrio fluv	346	11	2.0	85	10	040921	040921 pseudotsuga
274	13	2.4	185	2	0930J9	093qj9 vibrio fluv	347	11	2.0	90	2	08VLR8	08vlr8 mycobacteri
275	13	2.4	185	2	0930J8	093qj8 vibrio mets	348	11	2.0	94	2	09L664	09l664 mycobacteri
276	13	2.4	185	2	0930J7	093qj7 vibrio mml	349	11	2.0	98	2	09L673	09l673 mycobacteri
277	13	2.4	185	2	0930J6	093qj6 vibrio mml	350	11	2.0	98	2	09L672	09l672 mycobacteri
278	13	2.4	185	2	0930J5	093qj5 vibrio mml	351	11	2.0	98	2	09L671	09l671 mycobacteri
279	13	2.4	185	2	0930J4	093qj4 vibrio para	352	11	2.0	98	2	09L670	09l670 mycobacteri
280	13	2.4	185	2	0930J3	093qj3 vibrio para	353	11	2.0	98	2	09L666	09l666 mycobacteri
281	13	2.4	185	2	0930J2	093qj2 vibrio para	354	11	2.0	98	2	09L661	09l661 mycobacteri
282	13	2.4	185	2	0930J1	093qj1 vibrio para	355	11	2.0	98	2	09L660	09l660 mycobacteri
283	13	2.4	185	2	0930I9	093qj9 vibrio sp.	356	11	2.0	98	2	09L659	09l659 mycobacteri
284	13	2.4	185	2	0930I8	093qj8 vibrio sp.	357	11	2.0	99	2	09L657	09l657 mycobacteri
285	13	2.4	185	2	0930I7	093qj7 pleiomonas	358	11	2.0	107	2	P72164	P72164 pseudomonas
286	13	2.4	185	2	0930I6	093qj6 campylobact	359	11	2.0	107	2	P75021	P75021 pseudomonas
287	13	2.4	185	2	0930I5	093qj5 campylobact	360	11	2.0	113	2	09S672	09s672 chlamydia p
288	13	2.4	185	2	0930I4	093qj4 campylobact	361	11	2.0	114	2	09S5X5	09s5x5 mycobacteri
289	13	2.4	185	2	0930I3	093qj3 shigella bo	362	11	2.0	114	2	09S5A4	09s5a4 mycobacteri
290	13	2.4	185	2	0930I2	093qj2 shigella bo	363	11	2.0	114	2	09S5A1	09s5a1 mycobacteri
291	13	2.4	185	2	0930I1	093qj1 shigella fi	364	11	2.0	114	2	09S5A0	09s5a0 mycobacteri
292	13	2.4	185	2	0930I0	093qj0 shigella so	365	11	2.0	114	2	09S5A0	09s5a0 mycobacteri
293	13	2.4	185	2	0930I0	093qj0 shigella so	366	11	2.0	114	2	09S5A0	09s5a0 mycobacteri
294	13	2.4	185	2	0930I0	093qj0 shigella so	367	11	2.0	114	2	09S5A0	09s5a0 mycobacteri
295	13	2.4	185	2	0930I0	093qj0 shigella so	368	11	2.0	114	2	09S5A0	09s5a0 mycobacteri
296	13	2.4	185	2	0930I0	093qj0 shigella so	369	11	2.0	114	2	09S5A0	09s5a0 mycobacteri
297	13	2.4	185	2	0930I0	093qj0 shigella so	370	11	2.0	114	2	09S5A0	09s5a0 mycobacteri
298	13	2.4	185	2	0930I0	093qj0 shigella so	371	11	2.0	114	2	09S5A0	09s5a0 mycobacteri
299	13	2.4	185	2	0930I0	093qj0 shigella so	372	11	2.0	114	2	09S5A0	09s5a0 mycobacteri
300	13	2.4	186	2	08V0U8	08v0u8 prevotella	373	11	2.0	120	2	09A1S4	09a1s4 mycobacteri
301	13	2.4	186	2	08V0U6	08v0u6 prevotella	374	11	2.0	120	2	09A1S4	09a1s4 mycobacteri
302	13	2.4	186	2	08V0U5	08v0u5 bacteroides	375	11	2.0	120	2	09A1S4	09a1s4 mycobacteri
303	13	2.4	186	2	08V0U4	08v0u4 bacteroides	376	11	2.0	120	2	09A1S4	09a1s4 mycobacteri
304	13	2.4	186	2	08V0U3	08v0u3 bacteroides	377	11	2.0	120	2	09A1S4	09a1s4 mycobacteri
305	13	2.4	186	2	08V0U2	08v0u2 bacteroides	378	11	2.0	120	2	09A1S4	09a1s4 mycobacteri
306	13	2.4	186	2	08V0U1	08v0u1 bacteroides	379	11	2.0	120	2	09A1S4	09a1s4 mycobacteri
307	13	2.4	186	2	08V0U0	08v0u0 bacteroides	380	11	2.0	120	2	09A1S4	09a1s4 mycobacteri
308	13	2.4	186	2	08V0U0	08v0u0 bacteroides	381	11	2.0	120	2	09A1S4	09a1s4 mycobacteri

382	11	2.0	124	2	09AE4	09AE4 mycobacteri	455	11	2.0	184	2	034818	034818 staphylococ
383	11	2.0	125	2	09AE5	09AE5 mycobacteri	456	11	2.0	184	2	034972	034972 staphylococ
384	11	2.0	126	2	09AE6	09AE6 mycobacteri	457	11	2.0	186	2	08VV0	08VV0 flavobacter
385	11	2.0	127	2	09AE7	09AE7 mycobacteri	458	11	2.0	186	2	08VV7	08VV7 chrysobact
386	11	2.0	127	2	09AE9	09AE9 mycobacteri	459	11	2.0	186	2	08VJ7	08VJ7 bartgeyella
387	11	2.0	127	2	09AE5	09AE5 mycobacteri	460	11	2.0	196	2	09K15	09K15 bifidobacte
388	11	2.0	127	2	09AE5	09AE5 mycobacteri	461	11	2.0	196	2	09K16	09K16 bifidobacte
389	11	2.0	128	2	09AE4	09AE4 mycobacteri	462	11	2.0	196	2	09AGE4	09AGE4 bifidobacte
390	11	2.0	128	2	09AE3	09AE3 mycobacteri	463	11	2.0	196	2	09EY8	09EY8 flavobacter
391	11	2.0	129	2	09AE2	09AE2 mycobacteri	464	11	2.0	196	2	09EY3	09EY3 bifidobacte
392	11	2.0	130	2	09AE3	09AE3 mycobacteri	465	11	2.0	223	2	09U30	09U30 caenorhabd
393	11	2.0	132	2	09AE9	09AE9 mycobacteri	466	11	2.0	258	4	09U30	09U30 caenorhabd
394	11	2.0	132	2	09AE9	09AE9 mycobacteri	467	11	2.0	315	4	09A19	09A19 homo saplen
395	11	2.0	133	2	09AE6	09AE6 mycobacteri	468	11	2.0	343	5	09A19	09A19 aster yello
396	11	2.0	133	2	09AE4	09AE4 mycobacteri	469	11	2.0	501	5	06118	06118 cryptospori
397	11	2.0	133	2	09AE4	09AE4 mycobacteri	470	11	2.0	544	5	P90622	06118 leishmania
398	11	2.0	133	2	09AE5	09AE5 mycobacteri	471	11	2.0	560	16	08V58	P90622 trichomonas
399	11	2.0	133	2	09AE5	09AE5 mycobacteri	472	11	2.0	560	16	08V58	08V58 anaplasma sp
400	11	2.0	133	2	09AE5	09AE5 mycobacteri	473	11	2.0	566	5	097130	097130 leishmania
401	11	2.0	133	2	09AE5	09AE5 mycobacteri	474	11	2.0	594	5	097131	097131 leishmania
402	11	2.0	133	2	09AE5	09AE5 mycobacteri	475	11	2.0	639	5	0961V0	0961V0 diosiphila
403	11	2.0	133	2	09AE5	09AE5 mycobacteri	476	11	2.0	35	5	09EY6	09EY6 myzus persi
404	11	2.0	133	2	09AE5	09AE5 mycobacteri	477	11	2.0	49	2	09EY6	09EY6 streptomyc
405	11	2.0	133	2	09AE5	09AE5 mycobacteri	478	11	2.0	194	2	09K170	09K170 bifidobacte
406	11	2.0	133	2	09AE5	09AE5 mycobacteri	479	11	2.0	196	2	09K160	09K160 bifidobacte
407	11	2.0	133	2	09AE5	09AE5 mycobacteri	480	11	2.0	196	2	09EY8	09EY8 bifidobacte
408	11	2.0	133	2	09AE5	09AE5 mycobacteri	481	11	2.0	196	2	09K169	09K169 bifidobacte
409	11	2.0	133	2	09AE5	09AE5 mycobacteri	482	11	2.0	196	2	09K166	09K166 bifidobacte
410	11	2.0	133	2	09AE5	09AE5 mycobacteri	483	11	2.0	196	2	09K168	09K168 bifidobacte
411	11	2.0	133	2	09AE5	09AE5 mycobacteri	484	11	2.0	196	2	09K163	09K163 bifidobacte
412	11	2.0	133	2	09AE5	09AE5 mycobacteri	485	11	2.0	196	2	09K162	09K162 bifidobacte
413	11	2.0	133	2	09AE5	09AE5 mycobacteri	486	11	2.0	196	2	09K159	09K159 bifidobacte
414	11	2.0	133	2	09AE5	09AE5 mycobacteri	487	11	2.0	196	2	09K158	09K158 bifidobacte
415	11	2.0	133	2	09AE5	09AE5 mycobacteri	488	11	2.0	196	2	09EY8	09EY8 bifidobacte
416	11	2.0	133	2	09AE5	09AE5 mycobacteri	489	11	2.0	196	2	09EY8	09EY8 bifidobacte
417	11	2.0	133	2	09AE5	09AE5 mycobacteri	490	11	2.0	196	2	09EY8	09EY8 bifidobacte
418	11	2.0	133	2	09AE5	09AE5 mycobacteri	491	11	2.0	196	2	09EY8	09EY8 bifidobacte
419	11	2.0	133	2	09AE5	09AE5 mycobacteri	492	11	2.0	196	2	09EY8	09EY8 bifidobacte
420	11	2.0	133	2	09AE5	09AE5 mycobacteri	493	11	2.0	196	2	09EY8	09EY8 bifidobacte
421	11	2.0	133	2	09AE5	09AE5 mycobacteri	494	11	2.0	196	2	09EY8	09EY8 bifidobacte
422	11	2.0	133	2	09AE5	09AE5 mycobacteri	495	11	2.0	196	2	09EY8	09EY8 bifidobacte
423	11	2.0	133	2	09AE5	09AE5 mycobacteri	496	11	2.0	196	2	09EY8	09EY8 bifidobacte
424	11	2.0	133	2	09AE5	09AE5 mycobacteri	497	11	2.0	196	2	09EY8	09EY8 bifidobacte
425	11	2.0	133	2	09AE5	09AE5 mycobacteri	498	11	2.0	196	2	09EY8	09EY8 bifidobacte
426	11	2.0	133	2	09AE5	09AE5 mycobacteri	499	11	2.0	196	2	09EY8	09EY8 bifidobacte
427	11	2.0	133	2	09AE5	09AE5 mycobacteri	500	11	2.0	196	2	09EY8	09EY8 bifidobacte
428	11	2.0	133	2	09AE5	09AE5 mycobacteri	501	11	2.0	196	2	09EY8	09EY8 bifidobacte
429	11	2.0	133	2	09AE5	09AE5 mycobacteri	502	11	2.0	196	2	09EY8	09EY8 bifidobacte
430	11	2.0	133	2	09AE5	09AE5 mycobacteri	503	11	2.0	196	2	09EY8	09EY8 bifidobacte
431	11	2.0	133	2	09AE5	09AE5 mycobacteri	504	11	2.0	196	2	09EY8	09EY8 bifidobacte
432	11	2.0	133	2	09AE5	09AE5 mycobacteri	505	11	2.0	196	2	09EY8	09EY8 bifidobacte
433	11	2.0	133	2	09AE5	09AE5 mycobacteri	506	11	2.0	196	2	09EY8	09EY8 bifidobacte
434	11	2.0	133	2	09AE5	09AE5 mycobacteri	507	11	2.0	196	2	09EY8	09EY8 bifidobacte
435	11	2.0	133	2	09AE5	09AE5 mycobacteri	508	11	2.0	196	2	09EY8	09EY8 bifidobacte
436	11	2.0	133	2	09AE5	09AE5 mycobacteri	509	11	2.0	196	2	09EY8	09EY8 bifidobacte
437	11	2.0	133	2	09AE5	09AE5 mycobacteri	510	11	2.0	196	2	09EY8	09EY8 bifidobacte
438	11	2.0	133	2	09AE5	09AE5 mycobacteri	511	11	2.0	196	2	09EY8	09EY8 bifidobacte
439	11	2.0	133	2	09AE5	09AE5 mycobacteri	512	11	2.0	196	2	09EY8	09EY8 bifidobacte
440	11	2.0	133	2	09AE5	09AE5 mycobacteri	513	11	2.0	196	2	09EY8	09EY8 bifidobacte
441	11	2.0	133	2	09AE5	09AE5 mycobacteri	514	11	2.0	196	2	09EY8	09EY8 bifidobacte
442	11	2.0	133	2	09AE5	09AE5 mycobacteri	515	11	2.0	196	2	09EY8	09EY8 bifidobacte
443	11	2.0	133	2	09AE5	09AE5 mycobacteri	516	11	2.0	196	2	09EY8	09EY8 bifidobacte
444	11	2.0	133	2	09AE5	09AE5 mycobacteri	517	11	2.0	196	2	09EY8	09EY8 bifidobacte
445	11	2.0	133	2	09AE5	09AE5 mycobacteri	518	11	2.0	196	2	09EY8	09EY8 bifidobacte
446	11	2.0	133	2	09AE5	09AE5 mycobacteri	519	11	2.0	196	2	09EY8	09EY8 bifidobacte
447	11	2.0	133	2	09AE5	09AE5 mycobacteri	520	11	2.0	196	2	09EY8	09EY8 bifidobacte
448	11	2.0	133	2	09AE5	09AE5 mycobacteri	521	11	2.0	196	2	09EY8	09EY8 bifidobacte
449	11	2.0	133	2	09AE5	09AE5 mycobacteri	522	11	2.0	196	2	09EY8	09EY8 bifidobacte
450	11	2.0	133	2	09AE5	09AE5 mycobacteri	523	11	2.0	196	2	09EY8	09EY8 bifidobacte
451	11	2.0	133	2	09AE5	09AE5 mycobacteri	524	11	2.0	196	2	09EY8	09EY8 bifidobacte
452	11	2.0	133	2	09AE5	09AE5 mycobacteri	525	11	2.0	196	2	09EY8	09EY8 bifidobacte
453	11	2.0	133	2	09AE5	09AE5 mycobacteri	526	11	2.0	196	2	09EY8	09EY8 bifidobacte
454	11	2.0	133	2	09AE5	09AE5 mycobacteri	527	11	2.0	196	2	09EY8	09EY8 bifidobacte

528	9	1.7	580	5	096783	096783 plectus acu
529	8	1.5	44	4	097203	097203 brassica na
530	8	1.5	98	2	097652	097652 mycobacteri
531	8	1.5	131	16	097652	097652 mycobacteri
532	8	1.5	146	17	097652	097652 mycobacteri
533	8	1.5	156	2	097652	097652 mycobacteri
534	8	1.5	161	9	094821	094821 agrobacteri
535	8	1.5	180	2	094821	094821 agrobacteri
536	8	1.5	184	2	095337	095337 agrobacteri
537	8	1.5	184	2	095337	095337 agrobacteri
538	8	1.5	191	16	095337	095337 agrobacteri
539	8	1.5	197	16	095337	095337 agrobacteri
540	8	1.5	235	16	095337	095337 agrobacteri
541	8	1.5	235	16	095337	095337 agrobacteri
542	8	1.5	333	16	095337	095337 agrobacteri
543	8	1.5	333	16	095337	095337 agrobacteri
544	8	1.5	366	5	024830	024830 streptococ
545	8	1.5	391	2	095337	095337 agrobacteri
546	8	1.5	431	2	095337	095337 agrobacteri
547	8	1.5	431	2	095337	095337 agrobacteri
548	8	1.5	440	10	094821	094821 agrobacteri
549	8	1.5	473	3	095337	095337 agrobacteri
550	8	1.5	524	10	095337	095337 agrobacteri
551	8	1.5	536	5	015782	015782 entamoeba h
552	8	1.5	538	2	095444	095444 actinobact
553	8	1.5	544	17	097829	097829 thermoplas
554	8	1.5	549	17	097829	097829 thermoplas
555	8	1.5	549	17	097829	097829 thermoplas
556	8	1.5	792	4	098022	098022 pyrococcus
557	8	1.5	851	10	023524	023524 aradidopsi
558	8	1.5	1113	4	096894	096894 homo sapien
559	8	1.5	1249	5	095337	095337 agrobacteri
560	8	1.5	1278	4	084844	084844 homo sapien
561	8	1.5	1325	10	064533	064533 aradidopsi
562	8	1.5	1371	16	08X042	08X042 ralsionia s
563	8	1.5	1504	5	09V86	09V86 diosiphila
564	8	1.5	1975	5	09VCD1	09VCD1 diosiphila

ALIGNMENTS

RESULT 1						
ID	033733	PRELIMINARY:	PRT:	481 AA.		
AC	033733:					
DT	01-JAN-1998 (TREMblrel. 05, Created)					
DT	01-JAN-1998 (TREMblrel. 05, Last sequence update)					
DT	01-MAR-2002 (TREMblrel. 20, Last annotation update)					
DE	60 kDa chaperonin (Protein Cpn60) (GroEL protein) (Fragment).					
GN	GROEL.					
OS	Streptococcus pyogenes.					
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;					
OC	Streptococcaceae; Streptococcus.					
OX	NCBI_TaxID=1314;					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=serotype M49.					
RA	Pohl B., Podilelski A., Zarges I.;					
RL	Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.					
CC	-1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND					
CC	PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS					
CC	CONDITIONS (BY SIMILARITY).					
CC	-1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF					
CC	7 SUBUNITS (BY SIMILARITY).					
CC	-1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.					
CC	EMBL: X89336; CA61520.1;					
DR	HSP: P06139; IGR.					
DR	InterPro: IPR001844; Chaperonin_Cpn60.					
DR	InterPro: IPR002423; Cpn60_TCP-1.					
DR	PIfam: PF00118; Cpn60_TCP1.1.					
DR	PRINTS: PR00298; CHAPERONIN60.					
DR	PRINTS: PR00304; TCOMPLEXTCP1.					

DR	PROSITE: P500296; CHAPERONIN_CPN60.1.					
KW	ATP-binding; Chaperone.					
FT	NON_TER					
SEQUENCE	481 AA; 50496 MW; FA080B97CA7B6D11 CRC6;					
Query Match	55.8%; Score 304; DB 2; Length					
Best Local Similarity	100.0%; Pred. No. 2,4e-304;					
Matches 304; Conservative 0; Mismatches 0; Ind						
OY	222 DKVSNIDILPLLEEVLTNRPPLIADVDGEALPTLVLRKSTGVVAVKAPGCD 281					
DB	160 DKVSNIDILPLLEEVLTNRPPLIADVDGEALPTLVLRKSTGVVAVKAPGCD 219					
OY	282 RRRKMEIDIALTGGVITEDGLKDATPTALGAAKITVDKSTVIVEDSSSSEA 341					
DB	220 RRRKMEIDIALTGGVITEDGLKDATPTALGAAKITVDKSTVIVEDSSSSEA 279					
OY	342 NRALIKSOLETTSDPFRKLRKLRKAGVAVIKVGPETALKEKRLRIDALNAT 401					
DB	280 NRALIKSOLETTSDPFRKLRKLRKAGVAVIKVGPETALKEKRLRIDALNAT 339					
OY	402 RAAVEGIYAGGATLIVIEKVALEEGDDATGRNIVLRALPEPVQIALNGYEGSV 461					
DB	340 RAAVEGIYAGGATLIVIEKVALEEGDDATGRNIVLRALPEPVQIALNGYEGSV 399					
OY	462 VIKLKNRPAGTGFNAATGEVMDIKTGIIDPVKVRSAQNAAVASLITTEAVVANK 521					
DB	400 VIKLKNRPAGTGFNAATGEVMDIKTGIIDPVKVRSAQNAAVASLITTEAVVANK 459					
OY	522 PEPA 525					
DB	460 PEPA 463					

RESULT 2

ID	09L6F1	PRELIMINARY:	PRT:	184 AA.		
AC	09L6F1:					
DT	01-OCT-2000 (TREMblrel. 15, Created)					
DT	01-OCT-2000 (TREMblrel. 15, Last sequence update)					
DT	01-MAR-2002 (TREMblrel. 20, Last annotation update)					
DE	Cpn60 (Fragment).					
GN	CPN60.					
OS	Streptococcus pyogenes.					
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;					
OC	Streptococcaceae; Streptococcus.					
OX	NCBI_TaxID=1314;					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=ATCC19615.					
RA	Goh S.-H., Hill J.E., Hemmingsen S.M.;					
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.					
CC	EMBL: AF352806; AAF43084.1;					
DR	HSP: P45746; IGRV.					
DR	InterPro: IPR002423; Cpn60_TCP-1.					
DR	PIfam: PF00118; Cpn60_TCP1.1.					
DR	ATP-binding; Chaperone.					
FT	NON_TER					
FT	NON_TER					
SO	SEQUENCE 184 AA; 19819 MW; 27C23787A267C1F8 CRC64;					
Query Match	33.8%; Score 184; DB 2; Length 184;					
Best Local Similarity	100.0%; Pred. No. 6e-181;					
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						

```

OY 91 ATVLTQAIHDEGLKNTAGANPIGIRGIEATATAVEALKAIAPVSGKEAIAQVAAS 150
    |||||||
DB 1 ATVLTQAIHDEGLKNTAGANPIGIRGIEATATAVEALKAIAPVSGKEAIAQVAAS 60
OY 151 SRSKVGGEYISEAMERVNDGVITTEESRGHMETELEVEEGMOPDRGLSQYVNTDNEKV 210
    |||||||
DB 61 SRSKVGGEYISEAMERVNDGVITTEESRGHMETELEVEEGMOPDRGLSQYVNTDNEKV 120
OY 211 ADLENPFILITDKKVSNIODILPLEEVLKTNRPILLIADVDGEALPTLVINKRTGFN 270
    |||||||
DB 121 ADLENPFILITDKKVSNIODILPLEEVLKTNRPILLIADVDGEALPTLVINKRTGFN 180
OY 271 VYAV 274
    ||||
DB 181 VYAV 184

```

RESULT 3

08RJH4 PRELIMINARY; PRT: 159 AA.

```

AC 08RJH4;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE 60 kDa chaperonin Cpn60 (Fragment).
CN Cpn60.
OS Streptococcus dysgalactiae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 27957, ATCC 43078, 62, AND 74;
RA McDonald W.L., Deighton M.A., Fry B.N.;
RT "Phylogeny comparison of Streptococcus sp. associated with bovine
RT mastitis using 16S rRNA and newly sequenced HSP60 genes."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF485794; AAL96573.1; -
DR EMBL: AF485795; AAL96574.1; -
DR EMBL: AF485796; AAL96575.1; -
DR EMBL: AF485797; AAL96576.1; -
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 17216 MW; 079B14AF907433BE CRC64;

```

Query Match 28.6%; Score 156; DB 2; Length 159;
 Best Local Similarity 100.0%; Pred. No. 4e-152;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 101 EGLKNTAGANPIGIRGIEATATAVEALKAIAPVSGKEAIAQVAASRSKVGGEYI 160
    |||||||
DB 4 EGLKNTAGANPIGIRGIEATATAVEALKAIAPVSGKEAIAQVAASRSKVGGEYI 63
OY 161 SEAMERVNDGVITTEESRGHMETELEVEEGMOPDRGLSQYVNTDNEKVADLENPFILIT 220
    |||||||
DB 64 SEAMERVNDGVITTEESRGHMETELEVEEGMOPDRGLSQYVNTDNEKVADLENPFILIT 123
OY 221 TDKKVSNIODILPLEEVLKTNRPILLIADVDGEA 236
    |||||||
DB 124 TDKKVSNIODILPLEEVLKTNRPILLIADVDGEA 159

```

RESULT 4

093TK8 PRELIMINARY; PRT: 184 AA.

```

AC 093TK8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Cpn60 (Fragment).
CN Cpn60.
OS Streptococcus canis.

```

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1329;
 RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN-ATCC43496;
RA Goh S.H., Hill J.E., Hemmingsen S.M.;
RT "Streptococcus species characterized by cpn60 sequence."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF352804; AAK48855.1; -
DR InterPro: IPR002423; Cpn60/TCF-1.
DR Pfam: PF00118; Cpn60_TCF1; 1.
KW ATP-binding; Chaperone.
FT NON_TER 1
FT NON_TER 184
SQ SEQUENCE 184 AA; 19768 MW; 479C981163B1166E CRC64;

```

Query Match 25.9%; Score 141; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.4e-136;
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 101 EGLKNTAGANPIGIRGIEATATAVEALKAIAPVSGKEAIAQVAASRSKVGGEYI 160
    |||||||
DB 11 EGLKNTAGANPIGIRGIEATATAVEALKAIAPVSGKEAIAQVAASRSKVGGEYI 70
OY 161 SEAMERVNDGVITTEESRGHMETELEVEEGMOPDRGLSQYVNTDNEKVADLENPFILIT 220
    |||||||
DB 71 SEAMERVNDGVITTEESRGHMETELEVEEGMOPDRGLSQYVNTDNEKVADLENPFILIT 130
OY 221 TDKKVSNIODILPLEEVLKTNRPILLIADVDGEA 236
    |||||||
DB 131 TDKKVSNIODILPLEEVLKTNRPILLIADVDGEA 151

```

RESULT 5

08RJ42 PRELIMINARY; PRT: 159 AA.

```

AC 08RJ42;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE 60 kDa chaperonin Cpn60 (Fragment).
CN Cpn60.
OS Streptococcus uberis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1349;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 13387, ATCC 700407, 16, AND 33;
RA McDonald W.L., Deighton M.A., Fry B.N.;
RT "Phylogeny comparison of Streptococcus sp. associated with bovine
RT mastitis using 16S rRNA and newly sequenced HSP60 genes."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF485801; AAL96580.1; -
DR EMBL: AF485802; AAL96581.1; -
DR EMBL: AF485803; AAL96582.1; -
DR EMBL: AF485804; AAL96583.1; -
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 17275 MW; 9C456169FEC22AF CRC64;

```

Query Match 18.3%; Score 100; DB 2; Length 159;
 Best Local Similarity 100.0%; Pred. No. 2.4e-94;
 Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 130 LKAIAPVSGKEAIAQVAASRSKVGGEYISEAMERVNDGVITTEESRGHMETELEVE 189
    |||||||
DB 33 LKAIAPVSGKEAIAQVAASRSKVGGEYISEAMERVNDGVITTEESRGHMETELEVE 92
OY 190 GMPDRGLSQYVNTDNEKVADLENPFILITDKKVSNIQ 229
    |||||||
DB 93 GMPDRGLSQYVNTDNEKVADLENPFILITDKKVSNIQ 132

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RESULT 6
08RJG8      PRELIMINARY:      PRT:      159 AA.
AC 08RJG8;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 60 kDa chaperonin Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus parauberis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1348;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 13386, 21B, AND 25;
RA McDonald M.L., Deighton M.A., Fry B.N.;
RT "Phylogeny comparison of Streptococcus sp. associated with bovine mastitis using 16S rRNA and newly sequenced HSP60 genes."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF485798; AAL96577.1;
DR EMBL: AF485799; AAL96578.1;
DR EMBL: AF485800; AAL96579.1;
FT NON_TER      1
FT SEQUENCE      159 AA: 17313 MW; 110382BF8F70EFD CRC64;
SO

Query Match
Best Local Similarity 16.7%; Score 91; DB 2; Length 159;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 GKALIAOVAVSSRSSEKGEYISEAMERVNDGYITIEESRGHETELEVEGMOPDRGYL 198
DB 42 GKALIAOVAVSSRSSEKGEYISEAMERVNDGYITIEESRGHETELEVEGMOPDRGYL 101
QY 199 SOYVTDNEKRVADLENPFILITDKKYSNIO 229
DB 102 SOYVTDNEKRVADLENPFILITDKKYSNIO 132

RESULT 7
093TK4      PRELIMINARY:      PRT:      184 AA.
AC 093TK4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus porcinus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC43138;
RA Goh S.H., Hill J.E., Hemmingsen S.M.;
RT "Streptococcus species characterized by cpn60 sequence."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF352810; AAK48861.1;
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; cpn60_TCP1; 1.
KW ATP-binding; Chaperone.
FT NON_TER      1
FT SEQUENCE      184 AA: 19868 MW; DE048E8708C36177 CRC64;
SO

Query Match
Best Local Similarity 15.8%; Score 86; DB 2; Length 184;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 139 GKALIAOVAVSSRSSEKGEYISEAMERVNDGYITIEESRGHETELEVEGMOPDRGYL 198
DB 49 GKALIAOVAVSSRSSEKGEYISEAMERVNDGYITIEESRGHETELEVEGMOPDRGYL 108
QY 199 SOYVTDNEKRVADLENPFILITDKK 224
DB 109 SOYVTDNEKRVADLENPFILITDKK 134

RESULT 8
093TL2      PRELIMINARY:      PRT:      184 AA.
AC 093TL2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC19258;
RA Goh S.H., Hill J.E., Hemmingsen S.M.;
RT "Streptococcus species characterized by cpn60 sequence."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF352800; AAK48851.1;
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; cpn60_TCP1; 1.
KW ATP-binding; Chaperone.
FT NON_TER      1
FT SEQUENCE      184 AA: 19848 MW; ECC6BD9A5FAF745A CRC64;
SO

Query Match
Best Local Similarity 14.7%; Score 80; DB 2; Length 184;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 KEALIAOVAVSSRSSEKGEYISEAMERVNDGYITIEESRGHETELEVEGMOPDRGYL 199
DB 50 KEALIAOVAVSSRSSEKGEYISEAMERVNDGYITIEESRGHETELEVEGMOPDRGYL 109
QY 200 QYVTDNEKRVADLENPFIL 219
DB 110 QYVTDNEKRVADLENPFIL 129

RESULT 9
093TK9      PRELIMINARY:      PRT:      184 AA.
AC 093TK9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus vestibularis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC49124;
RA Goh S.H., Hill J.E., Hemmingsen S.M.;
RT "Streptococcus species characterized by cpn60 sequence."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF352803; AAK48854.1;
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; cpn60_TCP1; 1.
KW ATP-binding; Chaperone.
FT NON_TER      1

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FT NON_TER 184 184
SQ SEQUENCE 184 AA; 19864 MW; 8234EDBE164FC988 CRC64;

Query Match
Best Local Similarity 14.7%; Score 80; DB 2; Length 184;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 KEAIAOVAVSSRSKVGGEYISEAMERVNDGVITTEESRGHETELEVYEGMFDGKYL 199
DB 50 KEAIAOVAVSSRSKVGGEYISEAMERVNDGVITTEESRGHETELEVYEGMFDGKYL 109
QY 200 QYVTDNEKRVADLENPFIL 219
DB 110 QYVTDNEKRVADLENPFIL 129

RESULT 10
093TK7 PRELIMINARY; PRT; 184 AA.
AC 093TK7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus salivarius.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_Taxid=1304;
RN [1]
RP SEQUENCE FROM N.A.
RA Goh S.H., Hall J.E., Hemmingsen S.M.;
RT "Streptococcus species characterized by cpn60 sequence."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF352807; AAK48858.1;
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.1.
KW ATP-binding; Chapterone.
FT NON_TER 1 184
FT SEQUENCE 184 AA; 19864 MW; 8234EDBE164FC988 CRC64;

Query Match
Best Local Similarity 14.7%; Score 80; DB 2; Length 184;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 KEAIAOVAVSSRSKVGGEYISEAMERVNDGVITTEESRGHETELEVYEGMFDGKYL 199
DB 50 KEAIAOVAVSSRSKVGGEYISEAMERVNDGVITTEESRGHETELEVYEGMFDGKYL 109
QY 200 QYVTDNEKRVADLENPFIL 219
DB 110 QYVTDNEKRVADLENPFIL 129

RESULT 11
08RJ02 PRELIMINARY; PRT; 159 AA.
AC 08RJ02;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 60 kDa chaperonin Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_Taxid=1311;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-ATCC 13813, ATCC 27956, 13821-4, AND 13824-5;
RA McDonald W.L., Deligton M.A., Fry B.N.;

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RT "Phylogeny comparison of Streptococcus sp. associated with bovine
RT mastitis using 16S rRNA and newly sequenced HSP60 genes."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF485790; AAL96569.1;
DR EMBL: AF485791; AAL96570.1;
DR EMBL: AF485792; AAL96571.1;
DR EMBL: AF485793; AAL96572.1;
FT NON_TER 1 159
FT SEQUENCE 159 AA; 17391 MW; C6F4C7AB753864C CRC64;

Query Match
Best Local Similarity 14.3%; Score 78; DB 2; Length 159;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 IAQPVSGKEAIAOVAVSSRSKVGGEYISEAMERVNDGVITTEESRGHETELEVYEGM 192
DB 36 IAQPVSGKEAIAOVAVSSRSKVGGEYISEAMERVNDGVITTEESRGHETELEVYEGM 95
QY 193 FDRGYLSQVYVTDNEKRV 210
DB 96 FDRGYLSQVYVTDNEKRV 113

RESULT 12
093TK3 PRELIMINARY; PRT; 184 AA.
AC 093TK3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cpn60 (Fragment).
GN Cpn60.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_Taxid=1311;
RN [1]
RP SEQUENCE FROM N.A.
RA Goh S.H., Hall J.E., Hemmingsen S.M.;
RT "Streptococcus species characterized by cpn60 sequence."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF352811; AAK48862.1;
DR InterPro: IPR002423; Cpn60/TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.1.
KW ATP-binding; Chapterone.
FT NON_TER 1 184
FT SEQUENCE 184 AA; 20012 MW; D420BAEB24EBDFB CRC64;

Query Match
Best Local Similarity 14.3%; Score 78; DB 2; Length 184;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 IAQPVSGKEAIAOVAVSSRSKVGGEYISEAMERVNDGVITTEESRGHETELEVYEGM 192
DB 43 IAQPVSGKEAIAOVAVSSRSKVGGEYISEAMERVNDGVITTEESRGHETELEVYEGM 102
QY 193 FDRGYLSQVYVTDNEKRV 210
DB 103 FDRGYLSQVYVTDNEKRV 120

RESULT 13
09AME7 PRELIMINARY; PRT; 540 AA.
AC 09AME7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).
OS Streptococcus agalactiae.

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OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1311;
RN [1]
RP SEQUENCE FROM N.A.
RA Jwo-Pain C.;
RT *Cloning, sequencing, and characterization of 60 kDa Chaperonin gene
from Streptococcus agalactiae.*;
RL submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL: AF325222; AKI2938.1; -
DR HSSP: P06139; 1GRU.
DR InterPro: IPR001844; Chaperln_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1; 1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PROSITE: PS00296; CHAPERONIN60_CPN60; 1.
KW ATP-binding; Chaperone.
SQ SEQUENCE 540 AA; 57287 MW; F392085FCF919DD1 CRC64;

Query Match 14.3%; Score 78; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 3.7e-71;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 IAQVSGKRALIAQVAASRSSEKVGYSIEMERVNDGYITIEESRGMELEVEGMDQ 192
DB 133 IAQVSGKRALIAQVAASRSSEKVGYSIEMERVNDGYITIEESRGMELEVEGMDQ 192
QY 193 FDRGYLSQYMTWTDNKKV 210
DB 193 FDRGYLSQYMTWTDNKKV 210

RESULT 14
069135 PRELIMINARY; PRT; 184 AA.
AC 069135;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE 60 kDa chaperonin (fragment).
GN Cpn60.
OS Streptococcus infantae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1346;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC29178;
RX MEDLINE-98313012; PubMed-9650992;
RA Goh S.H., Driedger D., Gillett S., Low D.E., Hemmingsen S.M., Amos M.,
Chan D., Lovgren M., Willey B.M., Shaw C., Smith J.A.;
RT Streptococcus infantae, a human and animal pathogen: specific
identification by the chaperonin 60 gene identification method.*;
RL J. Clin. Microbiol. 36:2164-2166(1998).
DR EMBL: AF064076; AAC16861.1; -
DR HSSP: P45746; 1SRV.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1; 1.
KW ATP-binding; Chaperone.
FT NON_TER 1
FT NON_TER 184
SQ SEQUENCE 184 AA; 20009 MW; CE577F5CBA07E374 CRC64;

Query Match 13.8%; Score 75; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.7e-68;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 AIAQVAASRSSEKVGYSIEMERVNDGYITIEESRGMELEVEGMDQFDRGYLSQY 201
DB 52 AIAQVAASRSSEKVGYSIEMERVNDGYITIEESRGMELEVEGMDQFDRGYLSQY 111
QY 202 MYTDNEMKVAADLENP 216
DB 112 MYTDNEMKVAADLENP 126

RESULT 15
09X4R5
ID 09X4R5 PRELIMINARY; PRT; 540 AA.
AC 09X4R5;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).
GN GROEL.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CP1200;
RA Kim S.N., Lee J.Y., Kim S.W., Choi I.H., Rhee D.K.;
RT *GroEL sequences in Streptococcus pneumoniae.*;
RL submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL: AF117741; AAD23455.1; -
DR HSSP: P06139; 1GRU.
DR InterPro: IPR001844; Chaperln_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1; 1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PROSITE: PS00296; CHAPERONIN60_CPN60; 1.
KW ATP-binding; Chaperone.
SQ SEQUENCE 540 AA; 57213 MW; 4CDB489AF1C632DA CRC64;

Query Match 12.8%; Score 70; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 6.6e-63;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 NRPLLIADVDVGEALPLVLNKRGTFFNVAVKAPGDRKKAMLEDIALITGIVITE 301
DB 242 NRPLLIADVDVGEALPLVLNKRGTFFNVAVKAPGDRKKAMLEDIALITGIVITE 301
QY 302 DLGLELKDAT 311
DB 302 DLGLELKDAT 311

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